



SEQUENCE LISTING

<110> Nakamura, Yusuke
Furukawa, Yoichi

<120> Gene and Protein Relating to Hepatocellular Carcinoma and
Methods
of Use Thereof

<130> 25371-021 CIP

<140> US 10/788,847

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<150> 60/450,644

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<160> 83

<170> PatentIn version 3.2

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<213> Homo sapiens

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<221> CDS

<222> (96)..(1382)

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113

Met Glu Pro Leu Lys Val
1 5

gaa aag ttc gca acc gcc aac agg gga aac ggg ctg cgc gcc gtg acc
161

Glu Lys Phe Ala Thr Ala Asn Arg Gly Asn Gly Leu Arg Ala Val Thr
10 15 20

ccg ctg cgc ccc gga gag cta ctc ttc cgc tcg gat ccc ttg gcg tac
 209
 Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg Ser Asp Pro Leu Ala Tyr
 25 30 35

acg gtg tgc aag ggg agt cgt ggc gtc gtc tgc gac cgc tgc ctt ctc
 257
 Thr Val Cys Lys Gly Ser Arg Gly Val Val Cys Asp Arg Cys Leu Leu
 40 45 50

ggg aag gaa aag ctg atg cga tgc tct cag tgc cgc gtc gcc aaa tac
 305
 Gly Lys Glu Lys Leu Met Arg Cys Ser Gln Cys Arg Val Ala Lys Tyr
 55 60 65 70

tgt agt gct aag tgt cag aaa aaa gct tgg cca gac cac aag cgg gaa
 353
 Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp Pro Asp His Lys Arg Glu
 75 80 85

tgc aaa tgc ctt aaa agc tgc aaa ccc aga tat cct cca gac tcc gtt
 401
 Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg Tyr Pro Pro Asp Ser Val
 90 95 100

cga ctt ctt ggc aga gtt gtc ttc aaa ctt atg gat gga gca cct tca
 449
 Arg Leu Leu Gly Arg Val Val Phe Lys Leu Met Asp Gly Ala Pro Ser
 105 110 115

gaa tca gag aag ctt tac tca ttt tat gat ctg gag tca aat att aac
 497
 Glu Ser Glu Lys Leu Tyr Ser Phe Tyr Asp Leu Glu Ser Asn Ile Asn
 120 125 130

aaa ctg act gaa gat aag aaa gag ggc ctc agg caa ctc gta atg aca
 545
 Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu Arg Gln Leu Val Met Thr
 135 140 145 150

ttt caa cat ttc atg aga gaa gaa ata cag gat gcc tct cag ctg cca
 593
 Phe Gln His Phe Met Arg Glu Glu Ile Gln Asp Ala Ser Gln Leu Pro
 155 160 165

cct gcc ttt gac ctt ttt gaa gcc ttt gca aaa gtg atc tgc aac tct
 641
 Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala Lys Val Ile Cys Asn Ser
 170 175 180

ttc acc atc tgt aat gcg gag atg cag gaa gtt ggt gtt ggc cta tat
 689
 Phe Thr Ile Cys Asn Ala Glu Met Gln Glu Val Gly Val Gly Leu Tyr
 185 190 195

ccc agt atc tct ttg ctc aat cac agc tgt gac ccc aac tgt tcg att
 737

Pro Ser Ile Ser Leu Leu Asn His Ser Cys Asp Pro Asn Cys Ser Ile
 200 205 210
 gtg ttc aat ggg ccc cac ctc tta ctg cga gca gtc cga gac atc gag
 785
 Val Phe Asn Gly Pro His Leu Leu Leu Arg Ala Val Arg Asp Ile Glu
 215 220 225 230
 gtg gga gag gag ctc acc atc tgc tac ctg gat atg ctg atg acc agt
 833
 Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu Asp Met Leu Met Thr Ser
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 gag gag cgc cgg aag cag ctg agg gac cag tac tgc ttt gaa tgt gac
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 Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln Tyr Cys Phe Glu Cys Asp
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 tgt ttc cgt tgc caa acc cag gac aag gat gct gat atg cta act ggt
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 Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp Ala Asp Met Leu Thr Gly
 265 270 275
 gat gag caa gta tgg aag gaa gtt caa gaa tcc ctg aaa aaa att gaa
 977
 Asp Glu Gln Val Trp Lys Glu Val Gln Glu Ser Leu Lys Lys Ile Glu
 280 285 290
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 1025
 Glu Leu Lys Ala His Trp Lys Trp Glu Gln Val Leu Ala Met Cys Gln
 295 300 305 310
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 Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu Pro Asp Ile Asn Ile Tyr
 315 320 325
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 Gln Leu Lys Val Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu Gly
 330 335 340
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 Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr Arg Thr Met Glu Pro Tyr
 345 350 355
 agg att ttt ttc cca gga agc cat ccc gtc aga ggg gtt caa gtg atg
 1217
 Arg Ile Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met
 360 365 370
 aaa gtt ggc aaa ctg cag cta cat caa ggc atg ttt ccc caa gca atg
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 Lys Val Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met
 375 380 385 390

aag aat ctg aga ctg gct ttt gat att atg aga gtg aca cat ggc aga
1313

Lys Asn Leu Arg Leu Ala Phe Asp Ile Met Arg Val Thr His Gly Arg
395 400 405

gaa cac agc ctg att gaa gat ttg att cta ctt tta gaa gaa tgc gac
1361

Glu His Ser Leu Ile Glu Asp Leu Ile Leu Leu Leu Glu Glu Cys Asp
410 415 420

gcc aac atc aga gca tcc taa gggaacgcag tcagagggaa atacggcggtg
1412

Ala Asn Ile Arg Ala Ser
425

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1472

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35 40 45

Cys Asp Arg Cys Leu Leu Gly Lys Glu Lys Leu Met Arg Cys Ser Gln
50 55 60

Cys Arg Val Ala Lys Tyr Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp
65 70 75 80

Pro Asp His Lys Arg Glu Cys Lys Cys Leu Lys Ser Cys Lys Pro Arg

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Tyr Pro Pro Asp Ser Val Arg Leu Leu Gly Arg Val Val Phe Lys Leu		
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115	120	125
Leu Glu Ser Asn Ile Asn Lys Leu Thr Glu Asp Lys Lys Glu Gly Leu		
130	135	140
Arg Gln Leu Val Met Thr Phe Gln His Phe Met Arg Glu Glu Ile Gln		
145	150	155
Asp Ala Ser Gln Leu Pro Pro Ala Phe Asp Leu Phe Glu Ala Phe Ala		
165	170	175
Lys Val Ile Cys Asn Ser Phe Thr Ile Cys Asn Ala Glu Met Gln Glu		
180	185	190
Val Gly Val Gly Leu Tyr Pro Ser Ile Ser Leu Leu Asn His Ser Cys		
195	200	205
Asp Pro Asn Cys Ser Ile Val Phe Asn Gly Pro His Leu Leu Leu Arg		
210	215	220
Ala Val Arg Asp Ile Glu Val Gly Glu Glu Leu Thr Ile Cys Tyr Leu		
225	230	235
Asp Met Leu Met Thr Ser Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln		
245	250	255
Tyr Cys Phe Glu Cys Asp Cys Phe Arg Cys Gln Thr Gln Asp Lys Asp		
260	265	270
Ala Asp Met Leu Thr Gly Asp Glu Gln Val Trp Lys Glu Val Gln Glu		
275	280	285
Ser Leu Lys Lys Ile Glu Glu Leu Lys Ala His Trp Lys Trp Glu Gln		
290	295	300
Val Leu Ala Met Cys Gln Ala Ile Ile Ser Ser Asn Ser Glu Arg Leu		
305	310	315
		320

Pro Asp Ile Asn Ile Tyr Gln Leu Lys Val Leu Asp Cys Ala Met Asp
325 330 335

Ala Cys Ile Asn Leu Gly Leu Leu Glu Glu Ala Leu Phe Tyr Gly Thr
340 345 350

Arg Thr Met Glu Pro Tyr Arg Ile Phe Phe Pro Gly Ser His Pro Val
355 360 365

Arg Gly Val Gln Val Met Lys Val Gly Lys Leu Gln Leu His Gln Gly
370 375 380

Met Phe Pro Gln Ala Met Lys Asn Leu Arg Leu Ala Phe Asp Ile Met
385 390 395 400

Arg Val Thr His Gly Arg Glu His Ser Leu Ile Glu Asp Leu Ile Leu
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Leu Leu Glu Glu Cys Asp Ala Asn Ile Arg Ala Ser
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<211> 55

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<212> DNA

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20

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<222> (21)..(40)
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ctca
64

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31

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 <210> 42
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120

gcccgcgtct gaacctctcg cgccgccccg gccccagtgg aaagacgcgc aggcaaacg
180

caccacgtga cggagcgtga ccgcgcgcgc agcgcgcgcc aaggtcgggc aggaagaggg
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2760

caacatacga gccggaagca taaagtgtaa agcctggggg gcctaagag tgagctaact
2820

cacattaatt gcgttgcgct cactgcccgc tttccagtcg ggaaacctgt cgtgccagct
2880

gcattaatga atcgccaac gcgcggggag aggcgggttg cgtattgggc gctcttcgcg
2940

ttctcgtc actgactgc tgcgctcggc cgttcggctg cggcgagcgg tatcagctca
3000

ctcaaaggcg gtaatacggc tatccacaga atcaggggat aacgcaggaa agaacaatgtg
3060

agcaaaaggc cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca
3120

taggctccgc cccctgacg agcatcaca aaatcgacgc tcaagtcaga ggtggcgaaa
3180

cccgacagga ctataaagat accaggcggt tccccctgga agtccctcg tgcgctctcc
3240

tgttcgacc ctgccgtta ccggatacct gtccgccttt ctcccttcgg gaagcgtggc
3300

gctttctcat agtcacgct gtaggtatct cagttcgggt taggtcggtc gctccaagct
3360

gggctgtgtg cacgaacccc ccgttcagcc cgaccgctgc gccttatccg gtaactatcg
3420

tcttgagtcc aaccggtaa gacacgactt atcgccactg gcagcagcca ctggtaacag
3480

gattagcaga gcgaggtatg taggcgggtgc tacagagttc ttgaagtggg ggcctaacta
3540

cggctacact agaagaacag tatttggtat ctgcgctctg ctgaagccag ttaccttcgg
3600

aaaaagagtt ggtagctctt gatccggcaa acaaaccacc gctggtagcg gtttttttgt
3660

ttgcaagcag cagattacgc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc
3720

tacgggggtct gacgctcagt ggaacgaaaa ctacagttaa gggatttttg tcatgagatt
3780

atcaaaaagg atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta
3840

aagtatatat gagtaaactt ggtctgacag ttaccaatgc ttaatcagtg aggcacctat
3900

ctcagcgatc tgtctatttc gttcatccat agttgcctga ctccccgtcg tgtagataac
3960

tacgatacgg gagggcttac catctggccc cagtgtgca atgataccgc gagaccacg
4020

ctcaccggct ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag
4080

tggtcctgca actttatccg cctccatcca gtctattaat tggtgccggg aagctagagt
4140

aagtagttcg ccagttaata gtttgcgcaa cgttgttgcc attgctacag gcacgtgggt
4200

gtcacgctcg tcgtttggta tggcttcatt cagctccggt tcccaacgat caaggcgagt
4260

tacatgatcc cccatgttgt gcaaaaaagc ggtagctcc ttcggtctc cgatcgttgt
4320

cagaagtaag ttggccgcag tggtatcact catgggtatg gcagcactgc ataattctct
4380

tactgtcatg ccatccgtaa gatgcttttc tgtgactggg gagtactcaa ccaagtcatt
4440

ctgagaatag tgtatgcggc gaccgagttg ctcttgcccg gcgtcaatac gggataatac
4500

cgcgccacat agcagaactt taaaagtgct catcattgga aaacgttctt cggggcgaaa
4560

actctcaagg atcttaccgc tgttgagatc cagttcgatg taaccactc gtgcacccaa
4620

ctgatcttca gcatctttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca
4680

aaatgccgca aaaaagggaa taagggcgac acggaaatgt tgaatactca tactcttctt
4740

ttttcaatat tattgaagca tttatcaggg ttattgtctc atgagcggat acatatttga
4800

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4860

tgacgtc
4867

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Primer Sequence

<400> 45

ggggatcagc gtttgagtaa

20

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Primer Sequence

<400> 46
taggccccac ctccttctat
20

<210> 47
<211> 30
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<220>
<223> An Artificially Synthesized Primer Sequence

<400> 47
tgcggatcca gagcagattg tactgagagt
30

<210> 48
<211> 29
<212> DNA
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<220>
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<400> 48
ctctatctcg agtgaggcgg aaagaacca
29

<210> 49
<211> 40
<212> DNA
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<220>
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<400> 49
tttaagcttg aagactatctt ttacatcagg ttgtttttct
40

<210> 50
<211> 37
<212> DNA
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<220>
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<400> 50
tttaagcttg aagacacggt gtttcgtcct ttccaca
37

<210> 51
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Oligonucleotide Sequence

 <400> 51
 caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c
 51

 <210> 52
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Oligonucleotide Sequence

 <400> 52
 aaaagaagca gcacgacttc ttctctcttg aagaagaagt cgtgctgctt c
 51

 <210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Primer Sequence

 <400> 53
 ggggtaccag gatggagccg ctgaagggtgg
 30

 <210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Primer Sequence

 <400> 54
 gggaattctt aggatgctct gatgttggcg tcg
 33

 <210> 55
 <211> 51
 <212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 55

aaacttatgg atggagcacc tttcaagaga aggtgctcca tccataagtt t
51

<210> 56

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 56

aatcagagaa gctttactca tttcaagaga atgagtaaag cttctctgat t
51

<210> 57

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 57

aacaaactga ctgaagataa gttcaagaga cttatcttca gtcagtttgt t
51

<210> 58

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 58

aactcgtaat gacatttcaa cttcaagaga gttgaaatgt cattacgagt t
51

<210> 59

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 59
aaaagtgatc tgcaactctt tttcaagaga aaagagttgc agatcacttt t
51

<210> 60
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 60
aagtgatctg caactctttc attcaagaga tgaaagagtt gcagatcact t
51

<210> 61
<211> 51
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<220>
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<400> 61
aactctttca ccatctgtaa tttcaagaga attacagatg gtgaaagagt t
51

<210> 62
<211> 51
<212> DNA
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<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 62
aactgttcga ttgtgttcaa tttcaagaga attgaacaca atcgaacagt t
51

<210> 63
<211> 51
<212> DNA
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<400> 63
aaggatgctg atatgctaac tttcaagaga agttagcata tcagcatcct t
51

<210> 64
<211> 51
<212> DNA
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<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 64
aactggtgat gagcaagtat gttcaagaga catacttgct catcaccagt t
51

<210> 65
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 65
aagtatggaa ggaagttcaa gttcaagaga cttgaacttc cttccatact t
51

<210> 66
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 66
aacatctacc agctgaaggt gttcaagaga caccttcagc tggtagatgt t
51

<210> 67
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Hairpin siRNA Sequence

<400> 67
aagcaatgaa gaatctgaga cttcaagaga gtctcagatt cttcattgct t
51

<210> 68
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 68
 aaacttatgg atggagcacc t
 21

 <210> 69
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 69
 aatcagagaa gctttactca t
 21

 <210> 70
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 70
 aacaaactga ctgaagataa g
 21

 <210> 71
 <211> 21
 <212> DNA
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 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 71
 aactcgtaat gacatttcaa c
 21

 <210> 72
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 72

aaaagtgatc tgcaactctt t
21

<210> 73
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Target Sequence for siRNA

<400> 73
aagtgatctg caactctttc a
21

<210> 74
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 74
aactctttca ccatctgtaa t
21

<210> 75
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> An Artificially Synthesized Target Sequence for siRNA

<400> 75
aactgttcga ttgtgttcaa t
21

<210> 76
<211> 21
<212> DNA
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<220>
<223> An Artificially Synthesized Target Sequence for siRNA

<400> 76
aaggatgctg atatgctaac t
21

<210> 77

<211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 77
 aactggtgat gagcaagtat g
 21

 <210> 78
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 78
 aagtatggaa ggaagttcaa g
 21

 <210> 79
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> An Artificially Synthesized Target Sequence for siRNA

 <400> 79
 aacatctacc agctgaaggt g
 21

 <210> 80
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> An artificially Synthesized Target Sequence for siRNA

 <400> 80
 aagcaatgaa gaatctgaga c
 21

 <210> 81
 <211> 403
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> Homologous sequence of SEQ ID NO:1 and SEQ ID NO:82

<400> 81

Met Glu Leu Lys Val Glu Lys Phe Thr Ala Asn Arg Gly Asn Gly Leu
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Arg Ala Val Pro Leu Arg Pro Gly Glu Leu Leu Phe Arg Ser Asp Pro
20 25 30

Leu Ala Tyr Thr Val Cys Lys Gly Ser Arg Gly Val Val Cys Asp Arg
35 40 45

Cys Leu Leu Gly Lys Glu Lys Leu Met Arg Cys Ser Gln Cys Arg Ala
50 55 60

Lys Tyr Cys Ser Ala Lys Cys Gln Lys Lys Ala Trp Pro Asp His Arg
65 70 75 80

Glu Cys Cys Leu Lys Ser Cys Lys Pro Arg Tyr Pro Pro Asp Ser Val
85 90 95

Arg Leu Leu Gly Arg Val Lys Leu Met Asp Pro Ser Glu Ser Glu Lys
100 105 110

Leu Tyr Ser Phe Tyr Asp Leu Glu Ser Asn Ile Lys Leu Thr Glu Asp
115 120 125

Lys Lys Glu Gly Leu Arg Gln Leu Met Thr Phe Gln His Phe Met Arg
130 135 140

Glu Glu Ile Gln Asp Ala Ser Gln Leu Pro Pro Phe Asp Leu Phe Glu
145 150 155 160

Ala Phe Ala Lys Val Ile Cys Asn Ser Phe Thr Ile Cys Asn Ala Glu
165 170 175

Met Gln Glu Val Gly Val Gly Leu Tyr Pro Ser Ser Leu Leu Asn His
180 185 190

Ser Cys Asp Pro Asn Cys Ser Ile Val Phe Asn Gly Pro His Leu Leu
195 200 205

Leu Arg Ala Val Arg Ile Glu Gly Glu Glu Leu Thr Ile Cys Tyr Leu

210	215	220
Asp Met Leu Met Thr Ser Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln		
225	230	235 240
Tyr Cys Phe Glu Cys Asp Cys Arg Cys Gln Thr Gln Asp Lys Asp Ala		
	245	250 255
Asp Met Leu Thr Gly Asp Glu Gln Trp Lys Glu Val Gln Glu Ser Leu		
	260	265 270
Lys Lys Ile Glu Glu Leu Lys Ala His Trp Lys Trp Glu Gln Val Leu		
	275	280 285
Ala Cys Gln Ala Ile Ile Ser Asn Ser Arg Leu Pro Asp Ile Asn Ile		
	290	295 300
Tyr Gln Leu Lys Val Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu		
305	310	315 320
Gly Leu Glu Glu Ala Leu Phe Tyr Arg Thr Met Glu Pro Tyr Arg Ile		
	325	330 335
Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met Lys Val		
	340	345 350
Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met Lys Asn		
	355	360 365
Leu Arg Leu Ala Phe Asp Ile Met Val Thr His Gly Arg Glu His Ser		
	370	375 380
Leu Ile Glu Asp Leu Ile Leu Leu Leu Glu Glu Cys Asp Ala Asn Ile		
385	390	395 400

Arg Ala Ser

<210> 82
 <211> 428
 <212> PRT
 <213> Homo sapiens
 <400> 82

Met	Glu	Ala	Leu	Lys	Val	Glu	Lys	Phe	Thr	Thr	Ala	Asn	Arg	Gly	Asn	1	5	10	15
Gly	Leu	Arg	Ala	Val	Ala	Pro	Leu	Arg	Pro	Gly	Glu	Leu	Leu	Phe	Arg	20	25	30	
Ser	Asp	Pro	Leu	Ala	Tyr	Thr	Val	Cys	Lys	Gly	Ser	Arg	Gly	Val	Val	35	40	45	
Cys	Asp	Arg	Cys	Leu	Leu	Gly	Lys	Glu	Lys	Leu	Met	Arg	Cys	Ser	Gln	50	55	60	
Cys	Arg	Ile	Ala	Lys	Tyr	Cys	Ser	Ala	Lys	Cys	Gln	Lys	Lys	Ala	Trp	65	70	75	80
Pro	Asp	His	Arg	Arg	Glu	Cys	Ser	Cys	Leu	Lys	Ser	Cys	Lys	Pro	Arg	85	90	95	
Tyr	Pro	Pro	Asp	Ser	Val	Arg	Leu	Leu	Gly	Arg	Val	Ile	Val	Lys	Leu	100	105	110	
Met	Asp	Glu	Lys	Pro	Ser	Glu	Ser	Glu	Lys	Leu	Tyr	Ser	Phe	Tyr	Asp	115	120	125	
Leu	Glu	Ser	Asn	Ile	Ser	Lys	Leu	Thr	Glu	Asp	Lys	Lys	Glu	Gly	Leu	130	135	140	
Arg	Gln	Leu	Ala	Met	Thr	Phe	Gln	His	Phe	Met	Arg	Glu	Glu	Ile	Gln	145	150	155	160
Asp	Ala	Ser	Gln	Leu	Pro	Pro	Ser	Phe	Asp	Leu	Phe	Glu	Ala	Phe	Ala	165	170	175	
Lys	Val	Ile	Cys	Asn	Ser	Phe	Thr	Ile	Cys	Asn	Ala	Glu	Met	Gln	Glu	180	185	190	
Val	Gly	Val	Gly	Leu	Tyr	Pro	Ser	Met	Ser	Leu	Leu	Asn	His	Ser	Cys	195	200	205	
Asp	Pro	Asn	Cys	Ser	Ile	Val	Phe	Asn	Gly	Pro	His	Leu	Leu	Leu	Arg	210	215	220	

Ala Val Arg Glu Ile Glu Ala Gly Glu Glu Leu Thr Ile Cys Tyr Leu
 225 230 235 240

Asp Met Leu Met Thr Ser Glu Glu Arg Arg Lys Gln Leu Arg Asp Gln
 245 250 255

Tyr Cys Phe Glu Cys Asp Cys Ile Arg Cys Gln Thr Gln Asp Lys Asp
 260 265 270

Ala Asp Met Leu Thr Gly Asp Glu Gln Ile Trp Lys Glu Val Gln Glu
 275 280 285

Ser Leu Lys Lys Ile Glu Glu Leu Lys Ala His Trp Lys Trp Glu Gln
 290 295 300

Val Leu Ala Leu Cys Gln Ala Ile Ile Asn Ser Asn Ser Asn Arg Leu
 305 310 315 320

Pro Asp Ile Asn Ile Tyr Gln Leu Lys Val Leu Asp Cys Ala Met Asp
 325 330 335

Ala Cys Ile Asn Leu Gly Met Leu Glu Glu Ala Leu Phe Tyr Ala Met
 340 345 350

Arg Thr Met Glu Pro Tyr Arg Ile Phe Phe Pro Gly Ser His Pro Val
 355 360 365

Arg Gly Val Gln Val Met Lys Val Gly Lys Leu Gln Leu His Gln Gly
 370 375 380

Met Phe Pro Gln Ala Met Lys Asn Leu Arg Leu Ala Phe Asp Ile Met
 385 390 395 400

Lys Val Thr His Gly Arg Glu His Ser Leu Ile Glu Asp Leu Ile Leu
 405 410 415

Leu Leu Glu Glu Cys Asp Ala Asn Ile Arg Ala Ser
 420 425

<210> 83
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> An Artificially Synthesized Oligonucleotide Sequence

<400> 83

gcgggaggat ggagccgctg aaggtggaaa

30